

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/783,734ADATE: 05/01/1999
TIME: 07:48:57

INPUT SET: S31675.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Friedman, Jeffrey M.
Lee, Gwo-Hua
Proenca, Ricardo
Ioffe, Ella

(ii) TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC
ACIDS ENCODING THE RECEPTOR, AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 83

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: David A. Jackson, Esq.
(B) STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/783,734
(B) FILING DATE: 16-JAN-1997
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/599,974
(B) FILING DATE: 14-FEB-1996
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/586,594
(B) FILING DATE: 16-JAN-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Jackson Esq., David A.

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47 (B) REGISTRATION NUMBER: 26,742
48 (C) REFERENCE/DOCKET NUMBER: 600-1-162CP2
49
50 (ix) TELECOMMUNICATION INFORMATION:
51 (A) TELEPHONE: 201-487-5800
52 (B) TELEFAX: 201-343-1684
53
54
55 (2) INFORMATION FOR SEQ ID NO:1:
56
57 (i) SEQUENCE CHARACTERISTICS:
58 (A) LENGTH: 2529 base pairs
59 (B) TYPE: nucleic acid
60 (C) STRANDEDNESS: double
61 (D) TOPOLOGY: linear
62
63 (ii) MOLECULE TYPE: cDNA
64
65 (iii) HYPOTHETICAL: NO
66
67 (iv) ANTI-SENSE: NO
68
69
70 (vii) IMMEDIATE SOURCE:
71 (B) CLONE: A15 (OB-Ra)
72
73
74
75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
76
77 GGGCTCAGGT CGGCGTCGTA CCAGCCGCTG AAGCGGTTCT CCAGGTTCCA GGCGCTCTCG 60
78
79 CCATGCCGGA TCAGCACCAG CTTGTAGCTC GTGCCGAATT CGGCACGAGG TTGCTTTGGG 120
80
81 AATGAGCAAG GTCAAACTG CTCTGCACTC ACAGACAACA CTGAAGGGAA GACACTGGCT 180
82
83 TCAGTAGTGA AGGCTTCAGT TTTTCGCCAG CTAGGTGTAA ACTGGGACAT AGAGTGCTGG 240
84
85 ATGAAAGGGG ACTTGACATT ATTTCATCTGT CATATGGAGC CATTACCTAA GAACCCCTTC 300
86
87 AAGAATTATG ACTCTAAGGT CCATCTTTTA TATGATCTGC CTGAAGTCAT AGATGATTCTG 360
88
89 CCTCTGCCCC CACTGAAAGA CAGCTTTTCAG ACTGTCCAAT GCAACTGCAG TCTTCGGGGA 420
90
91 TGTGAATGTC ATGTGCCGGT ACCCAGAGCC AACTCAACT ACGCTCTTCT GATGTATTTG 480
92
93 GAAATCACAT CTGCCGGTGT GAGTTTTTCAG TCACCTCTGA TGTCAC TGCA GCCCATGCTT 540
94
95 GTTGTGAAAC CCGATCCACC CTTAGGTTTG CATATGGAAG TCACAGATGA TGGTAATTTA 600
96
97 AAGATTTCTT GGGACAGCCA AACAATGGCA CCATTTCCGC TTCAATATCA GGTGAAATAT 660
98
99 TTAGAGAATT CTACAATTGT AAGAGAGGCT GCTGAAATTG TCTCAGCTAC ATCTCTGCTG 720

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101	GTAGACAGTG	TGCTTCCTGG	ATCTTCATAT	GAGGTCCAGG	TGAGGAGCAA	GAGACTGGAT	780
102							
103	GGTTCAGGAG	TCTGGAGTGA	CTGGAGTTCA	CCTCAAGTCT	TTACCACACA	AGATGTTGTG	840
104							
105	TATTTTCCAC	CCAAAATTCT	GACTAGTGTT	GGATCGAATG	CTTCTTTTCA	TTGCATCTAC	900
106							
107	AAAAACGAAA	ACCAGATTAT	CTCCTCAAAA	CAGATAGTTT	GGTGGAGGAA	TCTAGCTGAG	960
108							
109	AAAATCCCTG	AGATACAGTA	CAGCATTTGTG	AGTGACCGAG	TTAGCAAAGT	TACCTTCTCC	1020
110							
111	AACCTGAAAG	CCACCAGACC	TCGAGGGAAG	TTTACCTATG	ACGCAGTGTA	CTGCTGCAAT	1080
112							
113	GAGCAGGCGT	GCCATCACCG	CTATGCTGAA	TTATACGTGA	TCGATGTCAA	TATCAATATA	1140
114							
115	TCATGTGAAA	CTGACGGGTA	CTTAACTAAA	ATGACTTGCA	GATGGTCACC	CAGCACAATC	1200
116							
117	CAATCACTAG	TGGGAAGCAC	TGTGCAGCTG	AGGTATCACA	GGCGCAGCCT	GTATTGTCCT	1260
118							
119	GATAGTCCAT	CTATTCATCC	TACGTCTGAG	CCCCAAAAC	GCGTCTTACA	GAGAGACGGC	1320
120							
121	TTTTATGAAT	GTGTTTTCCA	GCCAATCTTT	CTATTATCTG	GCTATACAAT	GTGGATCAGG	1380
122							
123	ATCAACCATT	CTTTAGGTTT	ACTTGACTCG	CCACCAACGT	GTGTCCTTCC	TGACTCCGTA	1440
124							
125	GTAAACCAC	TACCTCCATC	TAACGTAAAA	GCAGAGATTA	CTGTAAACAC	TGGATTATTG	1500
126							
127	AAAGTATCTT	GGGAAAAGCC	AGTCTTTCCG	GAGAATAACC	TTCAATTCCA	GATTCGATAT	1560
128							
129	GGCTTAAGTG	GAAAAGAAAT	ACAATGGAAG	ACACATGAGG	TATTCGATGC	AAAGTCAAAG	1620
130							
131	TCTGCCAGCC	TGCTGGTGTC	AGACCTCTGT	GCAGTCTATG	TGGTCCAGGT	TCGCTGCCGG	1680
132							
133	CGGTTGGATG	GACTAGGATA	TTGGAGTAAT	TGGAGCAGTC	CAGCCTATAC	GCTTGTCTATG	1740
134							
135	GATGTAAAAG	TTCTTATGAG	AGGGCCTGAA	TTTTGGAGAA	AAATGGATGG	GGACGTTACT	1800
136							
137	AAAAAGGAGA	GAAATGTCAC	CTTGCTTTGG	AAGCCCCCTGA	CGAAAAATGA	CTCACTGTGT	1860
138							
139	AGTGTGAGGA	GGTACGTGGT	GAAGCATCGT	ACTGCCCACA	ATGGGACGTG	GTCAGAAGAT	1920
140							
141	GTGGGAAATC	GGACCAATCT	CACTTTCCTG	TGGACAGAAC	CAGCGCACAC	TGTTACAGTT	1980
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143	CTGGCTGTCA	ATTCCTCGG	CGCTTCCCTT	GTGAATTTTA	ACCTTACCTT	CTCATGGCCC	2040
144							
145	ATGAGTAAAG	TGAGTGCTGT	GGAGTCACTC	AGTGCTTATC	CCCTGAGCAG	CAGCTGTGTC	2100
146							
147	ATCCTTTCCT	GGACACTGTC	ACCTGATGAT	TATAGTCTGT	TATATCTGGT	TATTGAATGG	2160
148							
149	AAGATCCTTA	ATGAAGATGA	TGGAATGAAG	TGGCTTAGAA	TTCCCTCGAA	TGTTAAAAAG	2220
150							
151	TTTTATATCC	ACGATAATTT	TATTCCCATC	GAGAAATATC	AGTTTAGTCT	TTACCCAGTA	2280
152							

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153 TTTATGGAAG GAGTTGGAAA ACCAAAGATA ATTAATGGTT TCACCAAAGA TGCTATCGAC 2340
154
155 AAGCAGCAGA ATGACGCAGG GCTGTATGTC ATTGTACCCA TAATTATTTTCTCTTGTGTC 2400
156
157 CTACTGCTCG GAACACTGTT AATTTACAC CAGAGAATGA AAAAGTTGTT TTGGGACGAT 2460
158
159 GTTCCAAACC CCAAGAAATTG TTCCTGGGCA CAAGGACTGA ATTTCCAAAA GAGAACGGAC 2520
160
161 ACTCTTTGA 2529
162

163 (2) INFORMATION FOR SEQ ID NO:2:

164 (i) SEQUENCE CHARACTERISTICS:

165 (A) LENGTH: 842 amino acids
166 (B) TYPE: amino acid
167 (C) STRANDEDNESS: Not Relevant
168 (D) TOPOLOGY: Not Relevant
169

170 (ii) MOLECULE TYPE: protein
171

172 (iii) HYPOTHETICAL: NO
173

174 (iv) ANTI-SENSE: NO
175

176 (vii) IMMEDIATE SOURCE:
177

178 (B) CLONE: OB-Ra
179
180
181
182

183 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

184
185 Gly Leu Arg Ser Ala Ser Tyr Gln Pro Leu Lys Arg Phe Ser Arg Phe
186 1 5 10 15
187
188 Gln Ala Leu Ser Pro Cys Arg Ile Ser Thr Ser Leu Xaa Leu Val Pro
189 20 25 30
190
191 Asn Ser Ala Arg Gly Cys Phe Gly Asn Glu Gln Gly Gln Asn Cys Ser
192 35 40 45
193
194 Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala Ser Val Val Lys
195 50 55 60
196
197 Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp Ile Glu Cys Trp
198 65 70 75 80
199
200 Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met Glu Pro Leu Pro
201 85 90 95
202
203 Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His Leu Leu Tyr Asp
204 100 105 110
205

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206	Leu	Pro	Glu	Val	Ile	Asp	Asp	Ser	Pro	Leu	Pro	Pro	Leu	Lys	Asp	Ser
207			115					120					125			
208																
209	Phe	Gln	Thr	Val	Gln	Cys	Asn	Cys	Ser	Leu	Arg	Gly	Cys	Glu	Cys	His
210		130					135					140				
211																
212	Val	Pro	Val	Pro	Arg	Ala	Lys	Leu	Asn	Tyr	Ala	Leu	Leu	Met	Tyr	Leu
213	145					150					155					160
214																
215	Glu	Ile	Thr	Ser	Ala	Gly	Val	Ser	Phe	Gln	Ser	Pro	Leu	Met	Ser	Leu
216					165					170					175	
217																
218	Gln	Pro	Met	Leu	Val	Val	Lys	Pro	Asp	Pro	Pro	Leu	Gly	Leu	His	Met
219			180						185					190		
220																
221	Glu	Val	Thr	Asp	Asp	Gly	Asn	Leu	Lys	Ile	Ser	Trp	Asp	Ser	Gln	Thr
222		195						200					205			
223																
224	Met	Ala	Pro	Phe	Pro	Leu	Gln	Tyr	Gln	Val	Lys	Tyr	Leu	Glu	Asn	Ser
225		210					215					220				
226																
227	Thr	Ile	Val	Arg	Glu	Ala	Ala	Glu	Ile	Val	Ser	Ala	Thr	Ser	Leu	Leu
228	225					230					235					240
229																
230	Val	Asp	Ser	Val	Leu	Pro	Gly	Ser	Ser	Tyr	Glu	Val	Gln	Val	Arg	Ser
231					245					250					255	
232																
233	Lys	Arg	Leu	Asp	Gly	Ser	Gly	Val	Trp	Ser	Asp	Trp	Ser	Ser	Pro	Gln
234			260						265					270		
235																
236	Val	Phe	Thr	Thr	Gln	Asp	Val	Val	Tyr	Phe	Pro	Pro	Lys	Ile	Leu	Thr
237		275						280					285			
238																
239	Ser	Val	Gly	Ser	Asn	Ala	Ser	Phe	His	Cys	Ile	Tyr	Lys	Asn	Glu	Asn
240		290					295					300				
241																
242	Gln	Ile	Ile	Ser	Ser	Lys	Gln	Ile	Val	Trp	Trp	Arg	Asn	Leu	Ala	Glu
243	305					310					315					320
244																
245	Lys	Ile	Pro	Glu	Ile	Gln	Tyr	Ser	Ile	Val	Ser	Asp	Arg	Val	Ser	Lys
246					325					330					335	
247																
248	Val	Thr	Phe	Ser	Asn	Leu	Lys	Ala	Thr	Arg	Pro	Arg	Gly	Lys	Phe	Thr
249				340					345					350		
250																
251	Tyr	Asp	Ala	Val	Tyr	Cys	Cys	Asn	Glu	Gln	Ala	Cys	His	His	Arg	Tyr
252		355						360					365			
253																
254	Ala	Glu	Leu	Tyr	Val	Ile	Asp	Val	Asn	Ile	Asn	Ile	Ser	Cys	Glu	Thr
255		370					375					380				
256																
257	Asp	Gly	Tyr	Leu	Thr	Lys	Met	Thr	Cys	Arg	Trp	Ser	Pro	Ser	Thr	Ile
258	385					390					395					400

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SEQUENCE VERIFICATION REPORT
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